

SEQUENCE LISTING

<110> Duke University
Arcasoy, Murat O.
Haroon, Zishan A.

<120> Use of Novel Cytokine Receptors as Biomarkers and Therapeutic Targets in Human Cancer

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<170> PatentIn version 3.1

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tggcgggggc tgtatcatgg accacctcgg ggcgtccctc tggccccagg tcggctccct 180
ttgtctcctg ctcgctgggg ccgcctggc gccccccct aacctccgg accccaaagt 240
cgagagcaaa gcggccttgc tggcggcccg ggggcccggaa gagcttctgt gcttcaccga 300
gcgggttggag gacttggtgt gtttctggga ggaagcggcg agcgctgggg tgggcccggg 360
caactacagc ttctcctacc agctcgagga tgagccatgg aagctgtgtc gcctgcacca 420

ggctcccacg	gctcggtgg	cggtgcgtt	ctgggtttcg	ctgcctacag	ccgacacgtc	480
gagttcgtg	cccctagagt	tgcggtcac	agcagcctcc	ggcgctccgc	gatatcaccg	540
tgtcatccac	atcaatgaag	tagtgctcct	agacgcccc	gtggggctgg	tggcgcggtt	600
ggctgacgag	agcggccacg	tagtggtcg	ctggctcccg	ccgcctgaga	cacccatgac	660
gtctcacatc	cgctacgagg	tggacgtctc	ggccggcaac	ggcgcaaggaa	gcgtacagag	720
ggtgagatc	ctggagggcc	gcaccgagtg	tgtgctgagc	aacctgcggg	gccggacgacg	780
ctacacccctc	gccgtcccg	cgcgtatggc	tgagccgagc	ttcggcggct	tctggagcgc	840
ctggtcggag	cctgtgtcgc	tgctgacgcc	tagcgacctg	gacccccc	tcctgacgct	900
ctccctcatc	ctcgtggta	tcctgggtct	gctgaccgtg	ctcgcgctgc	tctcccacccg	960
ccgggtctg	aagcagaaga	tctggcctgg	catcccggc	ccagagagcg	agtttgaagg	1020
cctttcacc	acccacaagg	gtaacttcca	gctgtggctg	taccagaatg	atggctgcct	1080
gtggtggagc	ccctgcaccc	ccttcacgga	ggacccaccc	gcttcctgg	aagtcccttc	1140
agagcgctgc	tggggacga	tgcaggcagt	ggagccgggg	acagatgatg	agggccccct	1200
gctggagcca	gtgggcagtg	agcatgccc	ggataccat	ctgggtgtgg	acaaatggtt	1260
gctggcccg	aacccgcccc	gtgaggaccc	cccaggccct	ggtggcagtg	tggacatagt	1320
ggccatggat	gaaggctcag	aagcatcctc	ctgctcatct	gctttggcct	cgaagcccg	1380
cccagaggga	gcctctgctg	ccagcttga	gtacactata	ctggacccca	gctccagct	1440
cttgcgtcca	tggacactgt	gccctgagct	gccccctacc	ccacccacc	taaagtacct	1500
gtaccttgtg	gtatctgact	ctggcatctc	aactgactac	agtcaggggg	actccaggg	1560
agcccaaggg	ggcttatccg	atggccccta	ctccaaccct	tatgagaaca	gccttatccc	1620
agccgctgag	cctctgcccc	ccagctatgt	ggcttgcct	taggacacca	ggctgcagat	1680
gatcagggat	ccaatatgac	tcaagagaacc	agtgcagact	caagacttat	ggaacaggaa	1740
tggcgaggcc	tctctcagga	gcagggccat	tgctgatttt	gtctgccc	tccatcctgc	1800
tcagggaaacc	acaacccctgc	agtatttta	aatatgtata	gttttttat	atgtatagtt	1860
ttttt						1865

<210> 4
 <211> 858
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (855)

<223> EpoR Isoform 1, intron 6 insert

<400> 4

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Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys	
1 5 10 15	
ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac	96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp	
20 25 30	
ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc ccg ggg ccc gaa	144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu	
35 40 45	
gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg	192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp	
50 55 60	
gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc	240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser	
65 70 75 80	
tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct	288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala	
85 90 95	
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc	336
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala	
100 105 110	
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc	384
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser	
115 120 125	
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc	432
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu	
130 135 140	
cta gac gcc ccc gtg ggg ctg gtg gcg ccg ttg gct gac gag agc ggc	480
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly	
145 150 155 160	
cac gta gtg ttg cgc tgg ctc ccg cct gag aca ccc atg acg tct	528
His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser	
165 170 175	
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc	576
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser	
180 185 190	
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc	624
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser	
195 200 205	
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg	672
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met	
210 215 220	
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg	720
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val	

225	230	235	240	
tcg ctg ctg acg cct agc gac ctg gac ccc ctc atc ctg acg ctc tcc Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser				768
245 250 255				
ctc atc ctc gtg gtc atc ctg gtg ctg ctg acc gtg ctc gcg ctg ctc Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu				816
260 265 270				
tcc cac cgc cgg atg gtc agg gaa ggc tcc agg agg agg tga Ser His Arg Arg Met Val Arg Glu Gly Ser Arg Arg Arg				858
275 280 285				
<210> 5				
<211> 285				
<212> PRT				
<213> Homo sapiens				
<400> 5				
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys 1 5 10 15				
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp 20 25 30				
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu 35 40 45				
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp 50 55 60				
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser 65 70 75 80				
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala 85 90 95				
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala 100 105 110				
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser 115 120 125				
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu 130 135 140				
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly 145 150 155 160				

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225 230 235 240

Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
260 265 270

Ser His Arg Arg Met Val Arg Glu Gly Ser Arg Arg Arg
275 280 285

<210> 6
<211> 954
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(951)
<223> EpoR Isoform 2, intron 7 insert

<400> 6
atg gac cac ctc ggg gcg tcc ctc tgg ccc cag gtc ggc tcc ctt tgt 48
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
1 5 10 15

ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac 96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30

ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc ccg ggg ccc gaa 144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45

gag ctt ctg tgc ttc acc gag cggtt gac ttgt gtgttgttttgg 192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60

gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser 65 70 75 80	240
tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala 85 90 95	288
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala 100 105 110	336
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser 115 120 125	384
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu 130 135 140	432
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly 145 150 155 160	480
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser 165 170 175	528
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser 180 185 190	576
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser 195 200 205	624
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met 210 215 220	672
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg Ala Glu Pro Ser Phe Gly Phe Trp Ser Ala Trp Ser Glu Pro Val 225 230 235 240	720
tcg ctg ctg acg cct agc gac ctg gac ccc ctc atc ctg acg ctc tcc Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser 245 250 255	768
ctc atc ctc gtg gtc atc ctg gtg ctg acc gtg ctc gcg ctg ctc Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu 260 265 270	816
tcc cac cgc cgg gct ctg aag cag aag atc tgg cct ggc atc ccg agc Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser 275 280 285	864
cca gag agc gag ttt gaa ggc ctc ttc acc acc cac aag ggt aac ttc Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe 290 295 300	912
cag gtt ggt gct att tct tca gct gtg gct gta cca gaa tga	954

Gln Val Gly Ala Ile Ser Ser Ala Val Ala Val Pro Glu
305 310 315

<210> 7
<211> 317
<212> PRT
<213> Homo sapiens

<400> 7

Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
1 5 10 15

Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30

Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65 70 75 80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
85 90 95

Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
100 105 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
115 120 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225 230 235 240

Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
260 265 270

Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
275 280 285

Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
290 295 300

Gln Val Gly Ala Ile Ser Ser Ala Val Ala Val Pro Glu
305 310 315

<210> 8
<211> 987
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(984)
<223> EpoR Isoform 3, intron 7 unspliced

<400> 8
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Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
1 5 10 15

ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac 96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30

ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc ccg ggg ccc gaa 144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45

gag ctt ctg tgc ttc acc gag cggtt gag gac ttgttgtttc tgg 192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60

gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc 240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65 70 75 80

tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct	288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala	
85 90 95	
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc	336
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala	
100 105 110	
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc	384
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser	
115 120 125	
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc	432
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu	
130 135 140	
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc	480
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly	
145 150 155 160	
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct	528
His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser	
165 170 175	
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc	576
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser	
180 185 190	
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc	624
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser	
195 200 205	
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg	672
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met	
210 215 220	
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg	720
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val	
225 230 235 240	
tcg ctg ctg acg cct agc gac ctg gac ccc ctc atc ctg acg ctc tcc	768
Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser	
245 250 255	
ctc atc ctc gtg gtc atc ctg gtg ctg ctg acc gtg ctc gcg ctg ctc	816
Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu	
260 265 270	
tcc cac cgc cgg gct ctg aag cag aag atc tgg cct ggc atc ccg agc	864
Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser	
275 280 285	
cca gag agc gag ttt gaa ggc ctc ttc acc acc cac aag ggt aac ttc	912
Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe	
290 295 300	
cag gta ggt ggc ctg gtt gtc ccc tca gtg cct ggg ctt ccc tgc ttc	960
Gln Val Gly Gly Leu Val Val Pro Ser Val Pro Gly Leu Pro Cys Phe	
305 310 315 320	

ttg cag cca aac tgc agg cct ctc tga
Leu Gln Pro Asn Cys Arg Pro Leu
325

987

<210> 9
<211> 328
<212> PRT
<213> Homo sapiens

<400> 9

Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
1 5 10 15

Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30

Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65 70 75 80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
85 90 95

Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
100 105 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
115 120 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser

195

200

205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
 210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
 225 230 235 240

Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
 245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
 260 265 270

Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
 275 280 285

Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
 290 295 300

Gln Val Gly Gly Leu Val Val Pro Ser Val Pro Gly Leu Pro Cys Phe
 305 310 315 320

Leu Gln Pro Asn Cys Arg Pro Leu
 325

<210> 10
 <211> 804
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(801)
 <223> EpoR Isoform 4, intron 5 unspliced

<400> 10
 atg gac cac ctc ggg gcg tcc ctc tgg ccc cag gtc ggc tcc ctt tgt 48
 Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
 1 5 10 15

ctc ctg ctc gct ggg gcc gcc tgg gcg ccc ccg cct aac ctc ccg gac 96
 Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
 20 25 30

ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc ccg ggg ccc gaa 144
 Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
 35 40 45

gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg 192
 Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp

50	55	60	
gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttgc tcc			240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser			
65 70 75 80			
tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct			288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala			
85 90 95			
ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc			336
Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala			
100 105 110			
gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc			384
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser			
115 120 125			
ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc			432
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu			
130 135 140			
cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc			480
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly			
145 150 155 160			
cac gta gtg ttg cgc tgg ctc ccg ccg cct gag aca ccc atg acg tct			528
His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser			
165 170 175			
cac atc cgc tac gag gtg gac gtc tcg gcc ggc aac ggc gca ggg agc			576
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser			
180 185 190			
gta cag agg gtg gag atc ctg gag ggc cgc acc gag tgt gtg ctg agc			624
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser			
195 200 205			
aac ctg cgg ggc cgg acg cgc tac acc ttc gcc gtc cgc gcg cgt atg			672
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met			
210 215 220			
gct gag ccg agc ttc ggc ggc ttc tgg agc gcc tgg tcg gag cct gtg			720
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val			
225 230 235 240			
tcg ctg ctg acg cct agc ggt gag gcc cca ggc ggg ggt gta gga gga			768
Ser Leu Leu Thr Pro Ser Gly Glu Ala Pro Gly Gly Val Gly Gly			
245 250 255			
gcc agg gcg aat cac ggg gca agc cca ccg ccc tga			804
Ala Arg Ala Asn His Gly Ala Ser Pro Pro Pro			
260 265			

<210> 11
 <211> 267
 <212> PRT
 <213> Homo sapiens

<400> 11

Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
1 5 10 15

Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
20 25 30

Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
35 40 45

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
50 55 60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65 70 75 80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
85 90 95

Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
100 105 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
115 120 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser
165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
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Ser Leu Leu Thr Pro Ser Gly Glu Ala Pro Gly Gly Gly Val Gly Gly
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 Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
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ccc aag ttc gag agc aaa gcg gcc ttg ctg gcg gcc ccg ggg ccc gaa 144
 Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
 35 40 45

gag ctt ctg tgc ttc acc gag cgg ttg gag gac ttg gtg tgt ttc tgg 192
 Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50 55 60

gag gaa gcg gcg agc gct ggg gtg ggc ccg ggc aac tac agc ttc tcc 240
 Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
 65 70 75 80

tac cag ctc gag gat gag cca tgg aag ctg tgt cgc ctg cac cag gct 288
 Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
 85 90 95

ccc acg gct cgt ggt gcg gtg cgc ttc tgg tgt tcg ctg cct aca gcc 336
 Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
 100 105 110

gac acg tcg agc ttc gtg ccc cta gag ttg cgc gtc aca gca gcc tcc 384
 Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
 115 120 125

ggc gct ccg cga tat cac cgt gtc atc cac atc aat gaa gta gtg ctc 432
 Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
 130 135 140

cta gac gcc ccc gtg ggg ctg gtg gcg cgg ttg gct gac gag agc ggc 480
 Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
 145 150 155 160

cac gta gtg ttg cgc tgg ctc ccg cct gag aca ccc atg acg tct 528

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser
180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
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Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
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